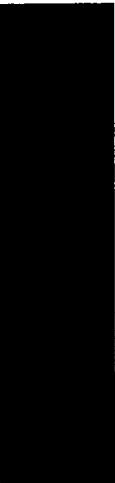


Sequence 1500 BP; 384 A; 472 C; 379 G; 265 T; 0 other;

Sequence 1500 BP; 384 A; 472 C; 379 G; 265 T; 0 other;

[illegible]

QY 1136 gcaaaagcgaaagaatcacaaatcaagccaagctggcgaacgcccgcgaacataccgcyg 1195
1136 gcaaaagcgaaagaatcacaaatcaagccaagctggcgaacgcccgcgaacataccgcyg 1195
QY 1196 catcatccaaaacagatgaagccccctacacccgaacagcaatccgtaagttctcgtcg 1255
1196 catcatccaaaacagatgaagccccctacacccgaacagcaatccgtaagttctcgtcg 1255
QY 1256 aatccgacggcattacccttcagacacataaccgaacagcagcgaacacacccctcgtcg 1315
1256 aatccgacggcattacccttcagacacataaccgaacagcagcgaacacacccctcgtcg 1315
Db 1316 tacgggtttccgacgcgcgagaacgcgcgagcttaagc 1354
1316 tacgggtttccgacgcgcgagaacgcgcgagcttaagc 1354



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alignment_scores:      Quality: 451.00      Length: 451
                       Ratio: 1.000      Gaps: 0
                       Percent Similarity: 100.000
alignment block:
US-09-388-050-3 x Y75748      ..
Align seg 1/1 to: Y75748 from: 1 to: 499

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Align seg 1/1 to: Y75748 from: 1 to: 499

See ID No. 3

March
Second report

SEE ID NO. 3

U.S. MAR 57

601 GTGCGTGCATCGCGCGCCCTTCGGCTTTGACACAGCTTGACCCCGG 650
|||||
201 ValAlaIaIleIleGlyAlaIleProheGlyPheAspAsnSerValThrAlaGl 217
|||||
651 CATCGTGTCCGCGCAAGCGAGAGCTGCCACGAAAGCTTACACACCTT 700
|||||
217 yIleValSerAlaIleGlyArgSerLeuProAsnIleSerTyrThrProp 234
|||||
701 TCATCCAAACCGACGCTTGCGATCATCCGGGCAATTCCGGGCGCGCTG 750
|||||
234 heIleGlnThrAspValAlaIleAsnProGlyAsnSerGlyGlyProLeu 250
|||||
751 TTCACCTTAAAGACAGCGCTCGCGCATCAATTCGCAAAATATACACCG 800
|||||
251 PheAsnLeuIleGlyIleValIleGlyIleAsnSerGlnIleTyrSerArg 267
|||||
801 CACCGCGCGATTCATGGGATCTCTTCGCGATCCGATTCGCGTTCGCA 850
|||||
851 gSerGlyGlyPheMetGlyIleSerPheAlaIleProIleAspValAlaIle 284
|||||
851 TGAATGTCCGCGCAACAGCTGAAAGACCGCGCAAGTCCAGCGGACAA 900
|||||
284 eIaAsnValAlaIleGlnIleLeuIleAsnThrGlyIleValIleGlnArgGlyGln 300
|||||
901 CTGGCGCGTATTCAGGAAGTATCTCAGGCTTCGCGACGCTCGTTCGCG 950
|||||
301 LeuGlyValIleIleGlnIleValIleSerTyrGlyLeuAlaIleGlnSerPheGln 317
|||||
951 TCTGGATTAAGCCAGCGCGCATTCGATTCGCAAAATCTTCGCGCGCACCC 1000
|||||
317 yLeuAspIleValIleSerGlyAlaIleLeuIleAlaIleValIleLeuProGlySerP 334
|||||
1001 CCGCAGAACGTCGCGCGCTCGCAGCGCGGCGACATCTCTTCAGCTTCGAC 1050
|||||
334 roAlaIleArgAlaIleGlyLeuGlnAlaIleGlyAspIleValIleLeuSerLeuAsp 350
|||||
1051 GCGCGAGAAATACCTTCTTCGCGGACCTCCCGTCATGCTCGCGCGCCAT 1100
|||||
351 GlyGlyGlyIleIleArgSerSerGlyAspLeuProValIleValIleValAlaIle 367
|||||
1101 TACCGCGGAAAGAAAGTCAAGCTTCGCGCTATGCGCGCAAGCCGCAAGAA 1150
|||||
367 eThrProGlyIleArgIleValIleSerLeuGlyValIleThrArgIleGlyIleGlnIle 384
|||||
1151 TCACAAATCAAGCCAAAGCTGGGCAAGCGCGCGAGCATACCGCGCATCA 1200
|||||
84 leThrIleIleValIleAlaIleGlyLeuGlyAsnAlaIleAlaIleIleThrGlyAlaIleSer 400
|||||
1201 TCCAAACACAGATGAAGCCCTTACACCGAAGCAATCCGCTACGTTTCG 1250
|||||
401 SerIleThrIleAspGlyAlaIleProIleThrGlnIleGlnIleSerGlyIleThrPhe 417
|||||
1251 GGTCAATCCGCGACGATTCACCTTCAGACACATACCGACACGCGCA 1300
|||||
417 yValIleIleSerAlaIleGlyIleThrIleGlnIleThrIleHisThrAspSerSerGlyIle 434
|||||
1301 AACACCTCGTGTCTGACGGGTTTCGAGCGGCGCAAGACGCGACGCTTA 1350
|||||
434 yHisIleIleValIleValIleArgValIleSerAspAlaIleAlaIleGlnArgAlaIleGlyLeu 450
|||||
1351 AGG 1353
|||||
451 Arg 451

II Search report

See ID NO. 3

seq documentation block:
ID 152994 standard; Protein: 499 AA.
AC Y52994;
DE 21-FEB-2000 (first entry)
DE Neisseria meningitidis strain ATCC 13090 BASB013 protein sequence.
KM Neisseria meningitidis; BASB013; diagnosis; infection; vaccine;
KW antibiotic; upper respiratory tract infection; bacteraemia; meningitis;
OS Neisseria meningitidis.
PN M0955872-A1.
04-NOV-1999.
20-APR-1999; 99MO-EP02765.
23-APR-1998; 98GB-0008734.
(SMK) SMITHKLINE BEECHAM BIOLOGICALS.
Ruelle J;
MPI; 2000-052809/04.
N-PSDB; 233306.
Novel polynucleotides and polypeptides from Neisseria meningitidis used to prepare vaccines against bacterial infections
Claim 3; Page 77-78; 94pp; English.
The present sequence represents a BASB013 polypeptide isolated from Neisseria meningitidis. BASB013 polynucleotides and polypeptides may be employed as research reagents and material for the discovery of treatments and diagnostics for diseases, particularly human diseases. They can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, or for screening of genetic mutations, serotype, organism or strain identification. Identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists (which are bacteriostatic) are used for the treatment and prevention of diseases such as upper respiratory tract infection, invasive bacterial diseases such as bacteraemia and meningitis, and in the development and screening of antibacterial drugs. They are also used on in-dwelling devices, or to extracellular matrix proteins thus prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.
Sequence 499 AA;

alignment scores:
Quality: 127.00
Ratio: 1.000

Length: 127
Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000
alignment block:
US-09-388-090-3 x Y52994
Align seg 1/1 10: Y52994 from: 1 to: 499

583 TTGAACCGGGCGAATGGCTGCGTCATCGCGCGCCCTTGCGCTTGA 632
195 LLeuLysProGlyGluTrpValAlaAlaIleGlyAlaProPheGlyPheAs 211
633 CAACACGCTGACCGCGCGCATGCTGCGCCCAAGCAGACGCTGCGCA 682
211 pAnserValThrAlaGlyIleValSerAlaLysGlyArgSerLeuProA 228
683 ACGAAGCTACACACCGCTTCATCAACCGACGCTGCGCATCAATCGCGGC 732
228 sngLysertyrThrProPheIleGlnThrAspValAlaIleAsnProGly 244
733 AATTCGGCGCGCCCGCTGTCACCTTAAAGACAGCTGTCGCGCATCA 782
245 AsnSerGlyGlyProLeuPheAsnLeuLysGlyIleValGlyIleAs 261
783 TTGCAAAATATACAGCGCGCGCGGATTCATGGCATCTCTTGCCA 832
261 nSerGlnIleTyrSerArgSerGlyGlyPheMetGlyIleSerPheAlaI 278
833 TCCTGATTCAGCTTCCTCATGATGTCGCGCAACAGCTGAATAAACCGGC 882
278 lProlIleAspValAlaIleMetAsnValAlaGlnIleLysAsnThrGly 294
883 AAAGTCACACCGCGCAACACTGCGCGTATTATTCAGGAAGTATCTACGG 932
295 LysValGlnArgGlyGlnLeuGlyValIleIleGlnIleValSerTyrGly 311
933 TTGCGACAGTCGCTGCGTCTGATTAAGCC 963
311 yLeuAlaGlnSerPheGlyLeuAspLysAla 321

seq name: ./3202.24acacata.499

seq_documentation_block:
; Sequence 8, Application PC/TUS9506211
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: ROCHALIMAEA HENSELAE AND ROCHALIMAEA QUINTANA INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

WO 9531549

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06211
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,294
; FILING DATE: 18 MAY 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.6121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-06211-8

alignment_scores:
Quality: 8.00 Length: 8
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-388-090-3 x PCT-US95-06211-8 ..
Align seg 1/1 to: PCT-US95-06211-8 from: 1 to: 503

640 GTGACCGCCGGCATCGTGTCGCC 663
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215 ValThrAlaGlyIleValSerAla 222